

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 16:12:05 ; Search time 39.8965 Seconds  
(without alignments)  
2810.909 Million cell updates/sec

Title: US-10-003-356-2  
Perfect score: 1138  
Sequence: 1 MFERRKEQDEGPGIHEFLAF.....RVIASDKIQSKAVVKRIQHF 219

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1138	100.0	755	2 Q8NGV9	Q8ngv9 homo sapien
2	740	65.0	912	2 O70410	O70410 mus musculus
3	613	53.9	476	2 Q8C0M6	Q8c0m6 mus musculus
4	547	48.1	618	2 Q8C0V4	Q8c0v4 mus musculus
5	362	31.8	940	2 O73635	O73635 fugu rubrip
6	360	31.6	940	2 Q90WL6	Q90wl6 sparus aura
7	354	31.1	850	2 Q6XAF2	Q6xaf2 salmo salar
8	354	31.1	941	2 Q6XAF1	Q6xaf1 salmo salar
9	354	31.1	941	2 Q6XAF3	Q6xaf3 salmo salar
10	353	31.0	1027	2 Q8J104	Q8j104 squalus aca
11	353	31.0	1078	1 CASR_HUMAN	P41180 homo sapien
12	353	31.0	1079	2 Q80ZA8	Q80za8 rattus norv
13	352	30.9	1079	1 CASR_MOUSE	Q9qy96 mus musculus
14	351	30.8	1079	1 CASR_RAT	P48442 rattus norv
15	349	30.7	1085	1 CASR_BOVIN	P35384 bos taurus
16	337	29.6	880	2 O73639	O73639 fugu rubrip
17	292.5	25.7	864	2 O73637	O73637 fugu rubrip
18	284.5	25.0	856	2 O73638	O73638 fugu rubrip
19	282	24.8	848	2 O93553	O93553 carassius a
20	281.5	24.7	844	2 O93552	O93552 carassius a
21	280	24.6	928	2 Q70VB1	Q70vb1 rattus norv
22	279.5	24.6	868	2 O73636	O73636 fugu rubrip
23	277	24.3	928	2 Q8K4Z6	Q8k4z6 mus musculus
24	276	24.3	751	2 Q6JK44	Q6jk44 homo sapien
25	276	24.3	855	2 Q6JK43	Q6jk43 homo sapien
26	276	24.3	926	2 Q8NHZ9	Q8nhz9 homo sapien
27	239.5	21.0	1218	2 Q90ZF3	Q90zf3 oncorhynchu
28	236.5	20.8	419	2 Q7SZW9	O7szw9 brachydanio
29	234.5	20.6	852	2 Q717C2	Q717c2 pan troglod
30	232.5	20.4	854	2 Q6UNX3	Q6unx3 ictalurus p
31	232	20.4	561	2 Q6NS58	Q6ns58 mus musculus

32	232	20.4	842	2 Q925I5	Q925i5 mus musculu
33	232	20.4	842	2 Q99PG5	Q99pg5 mus musculu
34	232	20.4	842	2 Q99PG6	Q99pg6 mus musculu
35	231.5	20.3	852	2 Q7RTX0	Q7rtx0 homo sapien
36	231.5	20.3	936	2 Q8NGW9	Q8ngw9 homo sapien
37	230.5	20.3	908	1 MGR8_HUMAN	O00222 homo sapien
38	230.5	20.3	908	1 MGR8_RAT	P70579 rattus norv
39	230.5	20.3	908	2 Q6B9F4	Q6b9f4 mus musculu
40	230	20.2	879	2 Q8NGU8	Q8ngu8 homo sapien
41	229.5	20.2	852	2 Q717C1	Q717c1 gorilla gor
42	229	20.1	1156	2 Q98UC6	Q98uc6 gallus gall
43	229	20.1	1188	2 Q98UC5	Q98uc5 gallus gall
44	229	20.1	1242	2 Q98UC4	Q98uc4 gallus gall
45	227	19.9	942	2 Q6J164	Q6j164 homo sapien

ALIGNMENTS

RESULT 1

Q8NGV9					
ID	Q8NGV9	PRELIMINARY;	PRT;	755 AA.	
AC	Q8NGV9;				
DT	01-OCT-2002 (TrEMBLrel. 22, Created)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DS	Seven transmembrane helix receptor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,				
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB065664; BAC05890.1; --				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	InterPro; IPR001828; ANF_receptor.				
DR	InterPro; IPR000337; GPCR_Mgr.				
DR	Pfam; PF00003; 7tm_3; 1.				
DR	Pfam; PF01094; ANF_receptor; 1.				
DR	PRINTS; PR00248; GPCRMR.				
DR	PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.				
KW	Receptor; Transmembrane.				
SQ	SEQUENCE 755 AA; 83791 MW; 04D56AD8917BDA1F CRC64;				

Query Match 100.0%; Score 1138; DB 2; Length 755;  
Best Local Similarity 100.0%; Pred. No. 5.8e-99;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFERRKEQDEGPGIHEFLAF	WAEIGSEAKBEKEERTCRL	LKGKCVDAENHSLVIGLFP	60
Db	1	MFERRKEQDEGPGIHEFLAF	WAEIGSEAKBEKEERTCRL	LKGKCVDAENHSLVIGLFP	60
Qy	61	IDSRTIPANESILEPASAKCEG	NFRFRWMMKAMHMIKEINKR	KDILPNITLGYQIFDT	120
Db	61	IDSRTIPANESILEPASAKCEG	NFRFRWMMKAMHMIKEINKR	KDILPNITLGYQIFDT	120
Qy	121	CFTISKSVEAVLVLTGQEENR	PNFRNSTGAPPAGIVGAGGS	FSLVPASRILGLYYLPQV	180
Db	121	CFTISKSVEAVLVLTGQEENR	PNFRNSTGAPPAGIVGAGGS	FSLVPASRILGLYYLPQV	180
Qy	181	GYTSTCVILSDKYQPPSYLR	VIASDKIQSKAVVKRIQHF	219	
Db	181	GYTSTCVILSDKYQPPSYLR	VIASDKIQSKAVVKRIQHF	219	

RESULT 2

O70410					
ID	O70410	PRELIMINARY;	PRT;	912 AA.	

```
AC 070410;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative pheromone receptor V2R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053986; AAC08413.1; -
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DFBFA48D CRC64;

Query Match 65.0%; Score 740; DB 2; Length 912;
Best Local Similarity 69.7%; Pred. No. 4.3e-61;
Matches 145; Conservative 25; Mismatches 30; Indels 8; Gaps 2;

Qy 17 FLAFLWAELGSEAKEKEEERTCRLGK-----CVDAENHSLVTGGLFPIDSRTPANES 71
Db 12 FLAFLWAVLGA--QNKTEEVQCRMAKNLSGYDAKNHSLVIAGLFFIHSRIIPVDEA 68
Qy 72 ILEPASAKCEGFNFRWKMAMHMIKEINRKRKILPNITLGVQIFDTCFTTISKSV EAV 131
Db 69 ILEPVSPMCEGFNFRWKMAMHMIKEINRKRKILPNHTLGVQIFDSCYTISKAMESS 128
Qy 132 LVFLTQGEENRPNFRNSTGAPGAGIVAGGSLFSLVPASRILGLYLPQVGYTSTCVILSD 191
Db 129 LVFLTQGEFEKFNERNSTGSTLAALVSGSGSLVAASRILGLYMPQVGYTSSCSILSD 188
Qy 192 KYQPPSYLRVIA SDKIQSKAVVKRIQHF 219
Db 189 KFQPPSYLRVLP SDNLQSEAIVNLIKHF 216

RESULT 3
Q8C0M6
ID Q8C0M6 PRELIMINARY; PRT; 476 AA.
AC Q8C0M6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933425M15 product:similar to PUTATIVE PHEROMONE
DE RECEPTOR V2R2, full insert sequence.
GN Name=4933425M15Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK030224; BAC26854.1; -
DR HSSP; P23385; LEWK.
DR MGD; MGI:2441693; 4933425M15Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00592; CASENSINGR.
```





```
OX NCBI_TaxID=31033;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=98226788; PubMed=9560249; DOI=10.1073/pnas.95.9.5178;
RA Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M.,
RA Nakanishi S., Brenner S.;
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
RT Fugu.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
DR EMBL; AB008857; BAA26122.1; -.
DR HSSP; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRMRGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 940 AA; 105813 MW; 06DAB7803B6878B3 CRC64;

Query Match 31.8%; Score 362; DB 2; Length 940;
Best Local Similarity 42.8%; Pred. No. 3.2e-25;
Matches 74; Conservative 37; Mismatches 56; Indels 6; Gaps 3;

QY 53 LVIGGLFPIDSRITIPANESI-LEPASAKCEGFNFRWKMAMIHMIKEINKRKDILPNI 111
Db ::::||||| :::: ||| ||| ||| ||| ||| ||| ||| ||| :||||
33 ILLGGLFPIHFGISSKDNLAARPESTKCVRFNFRGRWLQAMVFAIEEINNSSLPLNI 92
QY 112 TLGYQIFDTCFTISKVSVEAVLVLTGQE---ENRPNFRNSTGAFPA--GIVGAGGSFLSV 166
Db ||||:||||| |||:||||| : : ||| ||| ||| ||| ||| ||| ||| :|||
93 TLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNDEFNCCTDHIPATIAVVGAGSAVST 152
QY 167 PASRIILGLYLPQVGYTSTCVILSDKYQFPPSYLRVIAADKIQSKAVVKRIQHF 219
Db : : |||:||||| : : |||: ||| : : |||: ||| : : |||: ||| : : |||
153 AVANLLSLFYIPIQISYASSRLLSNKNQYKSFMRITPTDEHQATAMADVIEYF 205

RESULT 6
Q90WL6
ID Q90WL6 PRELIMINARY; PRT; 940 AA.
AC Q90WL6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Extracellular calcium sensing receptor.
GN Name=caar;
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21930045; PubMed=11932208;
RA Clark M.S., Bendell L., Power D.M., Warner S., Elgar G.,
RA Ingleton P.M.;
RT "Calcitonin: Characterisation and expression in a Teleost fish: Fugu
RT rubripes.";
RL J. Mol. Endocrinol. 28:111-123(2002).
DR EMBL; AJ289717; CAC41352.1; -.
DR HSSP; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
```

```
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRMRGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 940 AA; 105455 MW; 19C3CEDC75A0E3F9 CRC64;

Query Match 31.6%; Score 360; DB 2; Length 940;
Best Local Similarity 42.8%; Pred. No. 5e-25;
Matches 74; Conservative 36; Mismatches 57; Indels 6; Gaps 3;

QY 53 LVIGGLFPIDSRITIPANESI-LEPASAKCEGFNFRWKMAMIHMIKEINKRKDILPNI 111
Db ::::||||| :::: ||| ||| ||| ||| ||| ||| ||| ||| :||||
32 ILLGGLFPIHFGVASKDQDLAARPESSQCVRFNFRGRWLQAMIFAIDEINNSSTLLPNI 91
QY 112 TLGYQIFDTCFTISKVSVEAVLVLTGQE---ENRPNFRNSTGAFPA--GIVGAGGSFLSV 166
Db ||||:||||| |||:||||| : : ||| ||| ||| ||| ||| ||| ||| :|||
92 TLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNDEFNCCTDHIPATIAVVGAGSAVST 151
QY 167 PASRIILGLYLPQVGYTSTCVILSDKYQFPPSYLRVIAADKIQSKAVVKRIQHF 219
Db : : |||:||||| : : |||: ||| : : |||: ||| : : |||: ||| : : |||
152 AVANLLGLFYIPIQISYASSRLLSNKNQYKSFMRITPTDEYQATAMADIIEFF 204

RESULT 7
Q6XAF2
ID Q6XAF2 PRELIMINARY; PRT; 850 AA.
AC Q6XAF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium polyvalent cation receptor 3.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Nearing J.A., Harris W.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245444; AAP79924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRMRGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 850 AA; 96544 MW; 7E2B785FED3081B9 CRC64;

Query Match 31.1%; Score 354; DB 2; Length 850;
Best Local Similarity 41.6%; Pred. No. 1.6e-24;
Matches 72; Conservative 38; Mismatches 57; Indels 6; Gaps 3;

QY 53 LVIGGLFPIDSRITIPANESI-LEPASAKCEGFNFRWKMAMIHMIKEINKRKDILPNI 111
Db ::::||||| :::: ||| ||| ||| ||| ||| ||| ||| ||| :||||
32 ILLGGLFPMHFGVTSKDQDLAARPESTECVRYNFRGRWLQAMIFAIEEINNSSTLLPNI 91
QY 112 TLGYQIFDTCFTISKVSVEAVLVLTGQE---ENRPNFRNSTGAFPA--GIVGAGGSFLSV 166
Db ||||:||||| |||:||||| : : ||| ||| ||| ||| ||| ||| ||| :|||
```













```
FT CONFLICT 45 45 /FTID=VSP_002036.
FT CONFLICT 304 304 A -> S (in Ref. 2).
FT CONFLICT 410 410 L -> P (in Ref. 3).
FT CONFLICT 566 566 G -> D (in Ref. 2 and 3).
FT CONFLICT 595 595 V -> A (in Ref. 2).
FT CONFLICT 610 610 Y -> H (in Ref. 2, 3 and 5).
FT CONFLICT 814 814 E -> V (in Ref. 5).
FT CONFLICT 889 889 F -> L (in Ref. 5).
FT CONFLICT 906 909 L -> I (in Ref. 2).
FT CONFLICT 1057 1057 TGSN -> SGWI (in Ref. 2).
FT CONFLICT 1064 1064 V -> M (in Ref. 2).
FT CONFLICT 1076 1076 V -> A (in Ref. 2).
FT CONFLICT 1076 1076 I -> V (in Ref. 2).
SQ SEQUENCE 1079 AA; 120839 MW; AAF8BD472736D6E CRC64;

Query Match 30.9%; Score 352; DB 1; Length 1079;
Best Local Similarity 37.1%; Pred. No. 3.4e-24;
Matches 78; Conservative 44; Mismatches 64; Indels 24; Gaps 5;

QY 18 LAFLW--AELGSEAKEEKEERTCRLLGKCVDAENHSLVIGGLFPIDSRTPANESI-LE 74
Db 11 LALTWHSSAYGPDQRAQKGD-----IILGGLFPIHFGVAAKDQDLKSR 54

QY 75 PASAKCEGFNFRFMKAMIHMIKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134
Db 55 PESVECI RY NFRGRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEATLSF 114

QY 135 LTQGE---ENRPNFRNSTGAPPA--GIVGAGGSFLSVPASRIILGLYLPOVGYTSTCVIL 189
Db 115 VAQNKIDSLNLD EFCNCSEHIPSTIAVVGATSGVSTAVANLLGLFYIPQVSYASSRLL 174

QY 190 SDKYQPPSYLRVIASDKIQSKAVVKRIQHF 219
Db 175 SNKNQFKSFLRTIPNDEHQATAMADIIEYF 204

RESULT 14
CASR_RAT STANDARD; PRT; 1079 AA.
AC P48442;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (Casr) (Parathyroid
DE Cell calcium-sensing receptor).
GN Name=Casr; Synonyms=Gprc2a, Pcarl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney outer medulla;
RX MEDLINE=95116508; PubMed=7816802;
RA Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.;
RT "Cloning and functional expression of a rat kidney extracellular
RT calcium/polyvalent cation-sensing receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
RN [2]
RP SEQUENCE OF 1-294 FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=95241465; PubMed=7724534;
RA Ruat M., Snowman A.M., Snyder S.H.;
RT "Calcium sensing receptor: molecular cloning in rat and localization
RT to nerve terminals."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
CC -1- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC
```

```
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10354; AAC52149.1; -.
CC EMBL; U20289; AAC52195.1; -.
CC PIR; I59362; I59362.
CC HSSP; P23385; LEWK.
CC RGD; 2277; Casr.
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000068; Ca_sens_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1079 Extracellular calcium-sensing receptor.
FT DOMAIN 20 612 Extracellular (Potential).
FT TRANSMEM 613 635 1 (Potential).
FT DOMAIN 636 649 Cytoplasmic (Potential).
FT TRANSMEM 650 670 2 (Potential).
FT DOMAIN 671 681 Extracellular (Potential).
FT TRANSMEM 682 700 3 (Potential).
FT DOMAIN 701 724 Cytoplasmic (Potential).
FT TRANSMEM 725 745 4 (Potential).
FT DOMAIN 746 769 Extracellular (Potential).
FT TRANSMEM 770 792 5 (Potential).
FT DOMAIN 793 805 Cytoplasmic (Potential).
FT TRANSMEM 806 828 6 (Potential).
FT DOMAIN 829 836 Extracellular (Potential).
FT TRANSMEM 837 862 7 (Potential).
FT DOMAIN 863 1079 Cytoplasmic (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 130 130 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 261 261 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 287 287 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 386 386 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 446 446 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 468 468 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 541 541 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 594 594 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 1079 AA; 120867 MW; D7664550361F9736 CRC64;

Query Match 30.8%; Score 351; DB 1; Length 1079;
Best Local Similarity 36.7%; Pred. No. 4.3e-24;
Matches 77; Conservative 45; Mismatches 64; Indels 24; Gaps 5;

QY 18 LAFLW--AELGSEAKEEKEERTCRLLGKCVDAENHSLVIGGLFPIDSRTPANESI-LE 74
Db 11 LALAWHSSAYGPDQRAQKGD-----IILGGLFPIHFGVAAKDQDLKSR 54

QY 75 PASAKCEGFNFRFMKAMIHMIKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134
Db 55 PESVECI RY NFRGRWLQAMIFAIEEINSSPALLPNMTLGYRIFDTCNTVSKALEATLSF 114

QY 135 LTQGE---ENRPNFRNSTGAPPA--GIVGAGGSFLSVPASRIILGLYLPOVGYTSTCVIL 189
Db 115 VAQNKIDSLNLD EFCNCSEHIPSTIAVVGATSGVSTAVANLLGLFYIPQVSYASSRLL 174

QY 190 SDKYQPPSYLRVIASDKIQSKAVVKRIQHF 219
Db 175 SNKNQFKSFLRTIPNDEHQATAMADIIEYF 204
```

RESULT 15  
CASR\_BOVIN STANDARD; PRT; 1085 AA.  
AC P35384;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid  
DE Cell calcium-sensing receptor).  
GN Name=CASR; Synonyms=GPRC2A, PCAR1;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Parathyroid;  
RX MEDLINE=94077182; PubMed=8255296; DOI=10.1038/366575a0;  
RA Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O.,  
RA Sun A., Hediger M.A., Lytton J., Hebert S.C.;  
RT "Cloning and characterization of an extracellular Ca(2+)-sensing  
RT receptor from bovine parathyroid.";  
RL Nature 366:575-580(1993).  
CC -!- FUNCTION: Senses changes in the extracellular concentration of  
CC calcium ions. The activity of this receptor is mediated by a G-  
CC protein that activates a phosphatidylinositol-calcium second  
CC messenger system.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; S67307; AAB29171.1; -.  
DR PIR; S40476; S40476.  
DR HSSP; P23385; 1EWT.  
DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000068; Ca\_sens\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS50259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 1085 Extracellular calcium-sensing receptor.  
FT DOMAIN 20 613 Extracellular (Potential).  
FT TRANSMEM 614 636 1 (Potential).  
FT DOMAIN 637 650 Cytoplasmic (Potential).  
FT TRANSMEM 651 671 2 (Potential).  
FT DOMAIN 672 682 Extracellular (Potential).  
FT TRANSMEM 683 701 3 (Potential).  
FT DOMAIN 702 725 Cytoplasmic (Potential).  
FT TRANSMEM 726 746 4 (Potential).  
FT DOMAIN 747 770 Extracellular (Potential).  
FT TRANSMEM 771 793 5 (Potential).  
FT DOMAIN 794 806 Cytoplasmic (Potential).  
FT TRANSMEM 807 829 6 (Potential).  
FT DOMAIN 830 837 Extracellular (Potential).  
FT TRANSMEM 838 863 7 (Potential).  
FT DOMAIN 864 1085 Cytoplasmic (Potential).  
FT CARBOHYD 91 91 N-linked (GlcNAc..) (Potential).  
FT CARBOHYD 131 131 N-linked (GlcNAc..) (Potential).

FT	CARBOHYD	262	262	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	288	288	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	401	401	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	447	447	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	469	469	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	489	489	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	542	542	N-linked (GlcNAc..)	(Potential).
FT	CARBOHYD	595	595	N-linked (GlcNAc..)	(Potential).
SQ	SEQUENCE	1085	AA; 121170	MW; 5D66DE8C9CD13E47	CRC64;

Query Match 30.7%; Score 349; DB 1; Length 1085;  
Best Local Similarity 42.2%; Pred. No. 6.7e-24;  
Matches 73; Conservative 38; Mismatches 56; Indels 6; Gaps 3;

QY	53	LVIGGLFPIDSR	TIPANESI-LEPASAKCEGFNFRFRWKMAMHMKIKRDKDILPNI	111
Db	33	IILGGLFPIHFG	AVKDDLKSRPESVECI RYNGFRWLQAMIFAI EINS SPALLPNM	92
QY	112	TLGYQIFDTCFT	ISKSV EAVLVLTGQE---ENRPNFRNSTGAFPA--GIVGAGGSFLSV	166
Db	93	TLGYRIFDTCNT	VS KALEATLSFVAQNKIDSLNLDEFNCSEHIPSTIAVVGATSGGIST	152
QY	167	PASRILGLYYLP	QVGYTSTCVILSDKYQFPSPYLRLVIA SDKIQSKAVVKRIQHF	219
Db	153	AVANLLGLFYIP	QVSYASSRLLSNKNQKFSFLRTIPNDEHQATAMADIIEYF	205

Search completed: February 16, 2005, 16:36:43  
Job time : 40.8965 secs